Package ‘meshes’

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Title MeSH Enrichment and Semantic analyses
Version 1.28.0
Description MeSH (Medical Subject Headings) is the NLM controlled vocabulary used to manually index articles for MEDLINE/PubMed. MeSH terms were associated by Entrez Gene ID by three methods, gendoo, gene2pubmed and RBBH. This association is fundamental for enrichment and semantic analyses. meshes supports enrichment analysis (over-representation and gene set enrichment analysis) of gene list or whole expression profile. The semantic comparisons of MeSH terms provide quantitative ways to compute similarities between genes and gene groups. meshes implemented five methods proposed by Resnik, Schlicker, Jiang, Lin and Wang respectively and supports more than 70 species.

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Description

MeSH term enrichment analysis

Usage

enrichMeSH(
  gene,
  MeSHDb,
  database = "gendoo",
  category = "C",
  pvalueCutoff = 0.05,
  pAdjustMethod = "BH",
  universe,
  qvalueCutoff = 0.2,
  minGSSize = 10,
  maxGSSize = 500,
  meshdbVersion = NULL
)

Arguments

gene a vector of entrez gene id
MeSHDb MeSHDb
database one of 'gendoo', 'gene2pubmed' or 'RBBH'
geneSim

pvalueCutoff  Cutoff value of pvalue.
pAdjustMethod  one of "holm", "hochberg", "hommel", "bonferroni", "BH", "BY", "fdr", "none"
universe  background genes
qvalueCutoff  qvalue cutoff
minGSSize  minimal size of genes annotated by Ontology term for testing.
maxGSSize  maximal size of genes annotated for testing
meshdbVersion  version of MeSH.db. If NULL (the default), use the latest version.

Value

An enrichResult instance.

Author(s)

Guangchuang Yu

See Also

class?enrichResult

Examples

## Not run:
library(meshes)
library(AnnotationHub)
ah <- AnnotationHub()
qr_hsa <- query(ah, c("MeSHDb", "Homo sapiens"))
filepath_hsa <- qr_hsa[[1]]
db <- MeSHDbi::MeSHDb(filepath_hsa)
data(geneList, package="DOSE")
de <- names(geneList)[1:100]
x <- enrichMeSH(de, MeSHDb = db, database='gendoo', category = 'C')

## End(Not run)

geneSim  geneSim

description

semantic similarity between two gene vector

Usage

 geneSim(geneID1, geneID2 = NULL, measure = "Wang", combine = "BMA", semData)
Arguments

geneID1  gene ID vector

geneID2  gene ID vector

measure  one of "Wang", "Resnik", "Rel", "Jiang" and "Lin"

combine  One of "max", "avg", "rcmax", "BMA" methods, for combining semantic similarity scores of multiple DO terms associated with gene/protein.

semData  gene annotation data for semantic measurement

Value

score matrix

Author(s)

Guangchuang Yu

Examples

```r
## library(meshes)
## library(AnnotationHub)
## ah <- AnnotationHub()
## qr_hsa <- query(ah, c("MeSHDb", "Homo sapiens"))
## filepath_hsa <- qr_hsa[[1]]
## db <- MeSHDbi::MeSHDb(filepath_hsa)
## hsamd <- meshdata(db, category="A", computeIC=T, database="gendoo")
data(hsamd)
geneSim("241", "251", semData=hsamd, measure="Wang", combine="BMA")
```

Description

Gene Set Enrichment Analysis of MeSH

Usage

gseMeSH(

geneList,
MeSHDb,
database = "gendoo",
category = "C",
exponent = 1,
minGSSize = 10,
maxGSSize = 500,
eps = 1e-10,
pvalueCutoff = 0.05,
)
gseMeSH

    pAdjustMethod = "BH",
    verbose = TRUE,
    seed = FALSE,
    by = "fgsea",
    meshdbVersion = NULL,
    ...
)

Arguments

geneList      order ranked geneList
MeSHDb        MeSHDb
database      one of 'gendoo', 'gene2pubmed' or 'RBBH'
exponent      weight of each step
minGSSize     minimal size of each geneSet for analyzing
maxGSSize     maximal size of genes annotated for testing
eps           This parameter sets the boundary for calculating the p value.
pvalueCutoff  pvalue Cutoff
pAdjustMethod pvalue adjustment method
verbose       print message or not
seed          logical
by            one of 'fgsea' or 'DOSE'
meshdbVersion version of MeSH.db. If NULL (the default), use the latest version.
...           other parameter

Value

gseaResult object

Author(s)

Yu Guangchuang

Examples

## Not run:
library(meshes)
library(AnnotationHub)
ah <- AnnotationHub()
qr_hsa <- query(h, c("MeSHDb", "Homo sapiens"))
filepath_hsa <- qr_hsa[[1]]
db <- MeSHDbi::MeSHDb(filepath_hsa)
data(geneList, package="DOSE")
y <- gseMeSH(geneList, MeSHDb = db, database = 'gene2pubmed', category = "G")

## End(Not run)
Description

construct annoData for semantic measurement

Usage

meshdata(MeSHDb = NULL, database, category, computeIC = FALSE)

Arguments

MeSHDb    MeSHDb package
database   one of supported database
category   one of supported category
computeIC  logical value

Value

a GOSemSimDATA object

Author(s)

Guangchuang Yu

Examples

## Not run:
library(meshes)
library(AnnotationHub)
ah <- AnnotationHub()
qr_hsa <- query(ah, c("MeSHDb", "Homo sapiens"))
/filepath_hsa <- qr_hsa[[1]]
db <- MeSHDb::MeSHDb(filepath_hsa)
hsamd <- meshdata(db, category='A', computeIC=T, database="gendoo")

## End(Not run)
meshSim

Description

semantic similarity between two MeSH term vectors

Usage

meshSim(meshID1, meshID2, measure = "Wang", semData)

Arguments

- meshID1: MeSH term vector
- meshID2: MeSH term vector
- measure: one of "Wang", "Resnik", "Rel", "Jiang" and "Lin"
- semData: annotation data for semantic measurement, output by meshdata function

Value

score matrix

Author(s)

Guangchuang Yu [https://guangchuangyu.github.io](https://guangchuangyu.github.io)

Examples

```r
## library(meshes)
## library(AnnotationHub)
## ah <- AnnotationHub()
## qr_hsa <- query(ah, c("MeSHDb", "Homo sapiens"))
## filepath_hsa <- qr_hsa[[1]]
## db <- MeSHDbi::MeSHDb(filepath_hsa)
## hsamd <- meshdata(db, category='A', computeIC=T, database="gendoo")
## data(hsamd)
## meshSim("D000009", "D009130", semData=hsamd, measure="Resnik")
```

mesh_term_table

DATA Sets

Description

These datasets are used in meshes
**Description**

These objects are imported from other packages. Follow the links below to see their documentation.

**DOSE**  geneID, geneInCategory

**enrichplot**  cnetplot, dotplot, emapplot, gseaplot, heatplot, ridgeplot
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